REMARKS

Status of the Claims.

Claims 1, 4, 7, 10-11, 21-23, 26-28, 31, 33, 35-36, 44, 46-48, 62-66, 74-79, 93-94, 106-107, 113-116, and 118-119, 121-122, and 124-126 are pending in the instant application. Claims 3, 8, 14-18, 120 and 123 were rejected. Claims 1, 4, 7, 10-11, 21-23, 26-28, 31, 33, 35-36, 44, 46-48, 62-66, 74-79, 93-94, 106-107, 113-116, 118-119, 121-122, and 124-126 were allowed. Office Action, p. 7. Claims 3, 8, 14-18, 120, and 123 have been canceled herein without prejudice to subsequent renewal, including in a continuation or divisional application.

Rejection Under 35 USC § 112, First Paragraph.

Claims 3, 8, 14-18, 120, and 123 were rejected under 35 USC § 112, first paragraph, as allegedly failing to comply with the written description requirement. The Examiner takes the position that Applicants were not in possession of the claimed genus of nucleic acids defined by these claims because "[t]he evidence in the prior art supports the contention that the addition or absence of specific sequence within a CMV promoter can greatly alter function", citing Chapman *et al.*, *Nucleic Acids Res.* 19(14):3979 (1991) (specifically p. 3982, col. 2 last ¶) [hereinafter "Chapman"] and "[g]iven the vast size of the claimed genus of nucleic acid sequences that must correspond to the requisite functionality of equal or greater promoter activity as compared to reference CMV promoters,...the skilled artisan would not have been able to envision a sufficient number of specific embodiments embraced by the claims to describe the broadly claimed genus of nucleic acid structures." Office Action, p. 4.

This rejection is respectfully traversed as follows. The Examiner's argument that Chapman supports the contention that the addition or absence of nucleotides within a CMV promoter can greatly alter function is misplaced. Chapman disclosed that the inclusion of the first 400 base pairs of the *Pst* I fragment of the human CMV IE1 region in an expression plasmid yielded poor expression of glycoproteins in monkey kidney cells and Chinese hamster ovary cells. Chapman, supra, p. 3982, col. 2, last ¶. Deletion of these first 400 base pairs led to high levels of expression for several mammalian glycoproteins, suggesting a negative regulatory role for this region in the two cell types. *Id.*, p. 3983-3983, bridging ¶. The comparison of these findings in Chapman with claims 3, 8, 14-18, 120, and 123 is misplaced. The rejected claims are directed, e.g., to a genus of nucleic acids comprising a polynucleotide sequence that has at least 99% or 99.5% identity to SEQ ID NO:8

and promotes expression of an operably linked polypeptide-encoding nucleic acid at a level equal to or greater than that of a human CMV reference promoter. Given that SEQ ID NO:8 is 1767 nucleotides in length, a nucleotide sequence having at least 99% or 99.5% identity to SEQ ID NO:8 would differ from SEQ ID NO:8 by less than 17 or less than 9 nucleotides, respectively – far fewer nucleotides than the 400 nucleotides that Chapman eliminated from the CMV promoter sequence. Chapman's fragment nucleotide sequences in which 400 nucleotides have been removed from hCMV IE1 are not comparable to the nucleic acid sequences encompassed by the instant rejected claims, which differ from the polynucleotide sequence of SEQ ID NO:8, for example, by less than 17 nucleotides (e.g., claim 1) or 9 nucleotides (e.g., claim 7). The results in Chapman are not relevant to the claimed sequences.

Applicants also respectfully submit that the Examiner's contention that "[g]iven the vast size of the claimed genus of nucleic acid sequences that must correspond to the requisite functionality of equal or greater promoter activity as compared to reference CMV promoters,...the skilled artisan would not have been able to envision a sufficient number of specific embodiments embraced by the claims to describe the broadly claimed genus of nucleic acid structures" lacks merit. The genus defined by each rejected claim is specifically limited. Each rejected claim describes a genus of nucleic acids defined by specific structural features commonly possessed by members of the genus and correlated functional characteristics that are coupled with those structural features. Only those nucleic acids having the specified sequence identity and particular functionality fall within the claimed genus. For example, claim 3 specifies an isolated or recombinant nucleic acid comprising a polynucleotide sequence that has at least 99% sequence identity to the entire length of the polynucleotide sequence of SEQ ID NO:8 or the complementary polynucleotide sequence thereof, wherein the polynucleotide sequence promotes expression of a nucleic acid encoding a polypeptide to which the polynucleotide sequence is operably linked at a level that is equal to or greater than the level of expression of the polypeptide-encoding nucleic acid when it is operably linked to a wild-type human CMV promoter (e.g., SEQ ID NO:19 or SEQ ID NO:20). Claim 17, for example, which ultimately depends from claim 1, specifies more particularly that the nucleic acid promotes expression of the polypeptide-encoding nucleic acid at a level that is higher than the level when the polypeptide-encoding nucleic acid is linked to such human CMV promoter. The specification clearly describes such nucleic acids. For example, a nucleotide sequence comprising a sequence corresponding to clone 6A8 (SEQ ID NO:8) operably linked to a luciferase-encoding

sequence expressed luciferase at a substantially higher level than did the human Towne or AD169 CMV promoter in an *in vivo* luciferase assay.

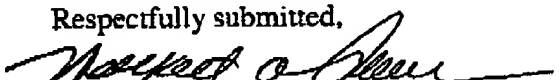
Based on Applicants' disclosure, one skilled in the art would have recognized that Applicants were in possession of the claimed nucleic acids because Applicants describe specific chemical structures having particular functions, disclose a specific correlation between the claimed structures and the asserted functions, and provide a specific description of the assays one can use to test whether a particular sequence has a specifically asserted function. For at least these reasons, Applicants respectfully submit that the rejection of claims 3, 8, 14-18, 120, and 123 is improper.

However, despite the fact that Applicants strongly disagree with the rejection, in an effort to expedite prosecution, Applicants have canceled claims 3, 8, 14-18, 120, and 123 herein without prejudice to subsequent renewal, including in a continuation or divisional application. Applicants specifically do not disavow any subject matter encompassed by claims 3, 8, 14-18, 120, and 123 and cancellation of these claims is not made for any reason relating to patentability of these claims.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested. If a telephone conference would expedite prosecution of this application in any way, the Examiner is invited to telephone the undersigned at (650) 298-5809.

Respectfully submitted,



Margaret A. Powers
Reg. No. 39,804

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Maxygen, Inc.
Intellectual Property Department
515 Galveston Drive
Redwood City, CA 94063
Telephone: 650-298-5809
Facsimile: 650-298-5446
Customer No.: 30560